IN THE CLAIMS:

1-21.(Cancelled)

22.(Original) A method for designing proteins comprising:

generating backbone protein configurations using a set of dihedral angle pairs;

eliminating self-intersecting configurations;

normalizing the total surface exposure of each remaining configuration;

generating a random set of sequences of hydrophobicities with uniform weight on the space allowed sequences for each remaining configuration;

determining, for each randomly generated sequence, which of the remaining configurations is the ground state;

recording the ground-state configuration for each sequence wherein desirable configurations are those containing the most sequences with that configuration as their ground state; and

synthesizing sequences of amino acids for the desirable configurations.

23.(Original) A method for designing proteins as in claim 22 wherein:

one set of dihedral angle pairs corresponds to an alpha helix and one set of dihedral angles corresponds to a beta strand.

24.(Original) A method for designing proteins as in claim 22 wherein:

two sets of dihedral angles correspond to an alpha helix and one set of dihedral angle pairs corresponds to a beta strand.

25.(Original) A method for designing proteins as in claim 24 wherein:

additional dihedral angle pairs fall within regions of high frequency in a Ramachandran plot.

26.(Original) A method for designing proteins as in claim 25 wherein:

the probability of choosing a particular pair of dihedral angles depends on the preceeding pairs of dihedral angles along the backbone.

27.(Cancelled)

28.(Currently Amended) A method for designing proteins as in claim 22 [[7]] further comprising:

eliminating non-compact configurations.

29.(Original) A method for designing proteins as in claim 28 further comprising:

clustering configurations sufficiently similar in the three dimensional trajectory followed by their backbones and treating all configurations within a cluster as variants of a single configuration, and;

summing, for all configurations in a cluster, the number of sequences with that configuration as their ground state such that the sum is considered the designability of the cluster.

30.(Original) A method for designing proteins as in claim 29 further comprising:

recording the Variance of each configuration, ranking the configurations from highest Variance to lowest, and

designing proteins starting with the configurations having the highest Variance.

31.(Original) A method for designing proteins as in claim 22 wherein:

the set of dihedral angles is a set of strings of dihedral angles.

32.(Original) A method for designing proteins as in claim 31 wherein:

the strings of angles are weighted according to their frequency of appearance in natural proteins and infrequent strings are eliminated.

33.(Original) A method for designing proteins as in claim 22 wherein:

normalizing is accomplished by dividing the surface exposure of each amino acid in a given configuration by the total surface exposure of that configuration.

34.(Original) A method for designing proteins as in claim 22 further comprising:

recording the Variance of each configuration, ranking the configurations from highest Variance to lowest, and

designing proteins starting with the configurations having the highest Variance.

35.(Original) A method for designing proteins as in claim 22 further comprising:

eliminating non-compact configurations after self-intersecting configurations are eliminated.

36.(Original) A method for designing proteins as in claim 35 further comprising:

clustering configurations sufficiently similar in the three dimensional trajectory followed by their backbones and treating all configurations within a cluster as variants of a single configuration, and;

summing, for all configurations in a cluster, the number of sequences with that configuration as their ground state such that the sum is considered the designability of the cluster.

37.(Original) A method for designing proteins as in claim 22 further comprising:

eliminating all configurations that are not favorable for forming hydrogen bonds after eliminating non-compact configurations.

38.(Original) A method for designing proteins as in claim 22 further comprising:

clustering configurations sufficiently similar in the three dimensional trajectory followed by their backbones and treating all configurations within a cluster as variants of a single configuration, and

summing, for all configurations in a cluster, the number of sequences with that configuration as their ground state such that the sum is considered the designability of the cluster.

39.(Original) A method for designing proteins as in claim 38 wherein:

clustering is accomplished by totaling the root-mean-square distance between every pair of configurations and defining a configuration as a member of a cluster if it lies within a root-mean-square distance λ of any member o the cluster.

40.(Original) A method for designing proteins as in claim 39 wherein:

λ is 0.4 Angstroms per amino acid.

41-57.(Cancelled)